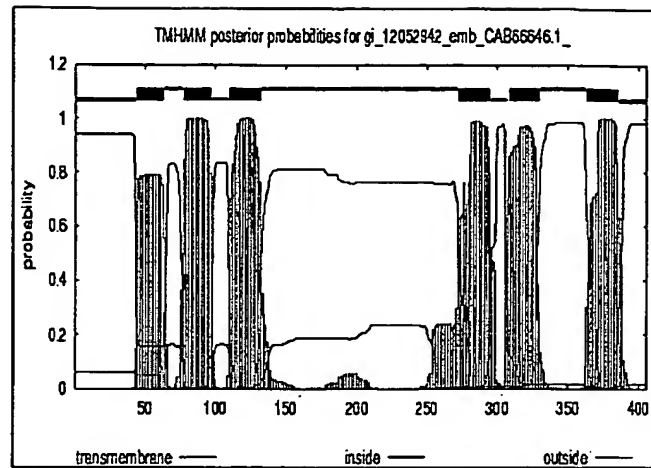


FIG. 1



CDS Prediction Server for Transmembrane Proteins

# gi\_12052942\_emb\_CAB66646.1 Length: 406  
 # gi\_12052942\_emb\_CAB66646.1 Number of predicted TMHs: 6  
 # gi\_12052942\_emb\_CAB66646.1 Exp number of AAs in TMHs: 132.21029  
 # gi\_12052942\_emb\_CAB66646.1 Exp number, first 60 AAs: 13.48568  
 # gi\_12052942\_emb\_CAB66646.1 Total prob of N-in: 0.94086  
 # gi\_12052942\_emb\_CAB66646.1 POSSIBLE N-term signal sequence

gi\_12052942\_emb\_CAB66646.1 TMHMM2.0inside 1 43  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 44 63  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0outside 64 77  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 78 97  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0inside 98 109  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 110 132  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0outside 133 272  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 273 295  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0inside 296 307  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 308 330  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0outside 331 362  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0TMhelix 363 385  
 gi\_12052942\_emb\_CAB66646.1 TMHMM2.0inside 386 406

FIG. 2

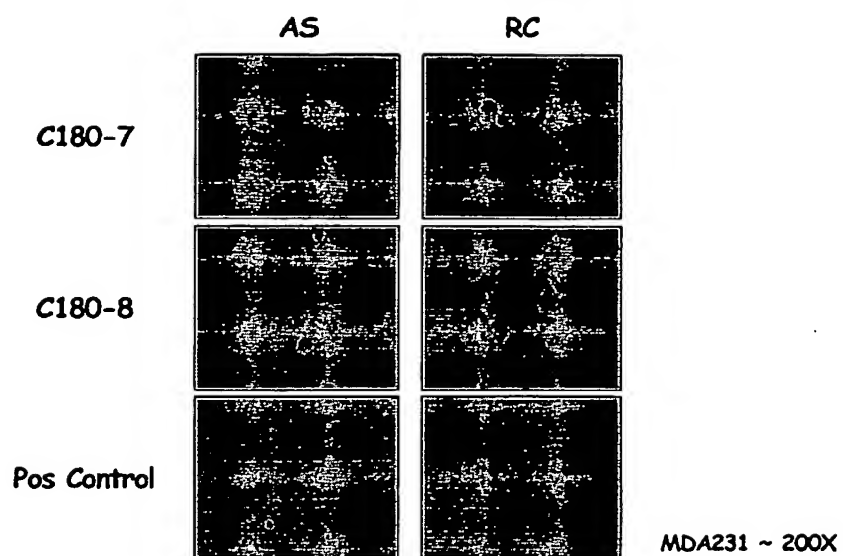


FIG. 3

		935		984
VMP1	(935)	TGGAATAACGTGTCGAGACTTTCTGGTACCTTTTGGACCTTCCTTGGG		
22793	(1)	-AGAAATTTGAGCAGTTCTGTGTTTATATTTTATT-CTCTTCTCTATC		
26883	(1)	---TAGAAGAGCTAACCTCACAGTCACACACCTAAAC--TAGGTCAT		
Consensus	(935)	GAATAACAGCTG CTCT ACT TACCTTTTT ACCTT T TGAT		
		985		1034
VMP1	(985)	CAA-CCCTAATTGGAAAGCAATATATAAAATGCATATCCAGAAATTTT		
22793	(49)	CAATCCCTGCCCTTTTGTAGTCCAGGTGGTAAGTACATTTCTTTAACGTTT		
26883	(46)	CAATCACTGATTTTACATCCAAACAAAGTGAAATCTGATAGTTGGGGTGA		
Consensus	(985)	CAA CCCTGATTTTA A CAA AA GTAAAT CAT TTC TTA TTTT		
		1035		1084
VMP1	1034)	TGTTATATATAACATTCAGCAAGCACA-DAGTG---GAGCAATCGTGGG		
22793	(99)	ATCCTCTCTTTCTCTCCCAATATGTGTC-TTTTCTTTTGGCTACTGACCC		
26883	(95)	AAAAGCAGAGTAAGGAGTTTTCAGAGTACTTGGGGTTTCTTACTTTTCA		
Consensus	(1035)	T GA T TCAT CAGAATGCA A TAGTT G GCTAATGTT CC		
		1085		1134
VMP1	(1079)	TTTCAATCTGCTCTGTCCTCCCATAGGTCCATCTCTGCAGAAAGCCATTTC		
22793	(148)	TCCTTCCAGTCTCTGTCCTCCCATAGGTCCATCTCTGCAGAAAGCCATTTC		
26883	(145)	TTT-TTTAATCTCTTCTAGGTTTTGTAACTTACAGACTTCA--AGG-ATTAT		
Consensus	(1085)	TTT TTAGTGCTGTCCCGGCATAGGTCCATCTCTGCAGAAAGCCATTTC		
		1135		1184
VMP1	1129)	AGGACTACCTGGAGGCTCAACGGCA-----GAAGC-TTCACACAAAAGC		
22793	(198)	AGGACTACCTGGAGGCTCAACGGCA-----GAAGC-TTCACACAAAAGC		
26883	(190)	AGATGATCTCTTTTACTACTTAATTAAGCTTTTTCATTGCTTT		
Consensus	(1135)	AGGACTACCTGGAGGCTCAACGGCA GAAGC TTCACACAAAAGC		
		1185		1234
VMP1	1173)	CAAAATGGGCACA---CCAGAGGAGAAAGCTGCTTCTCTGATCTTGA		
22793	(242)	CAAAATGGGCACA---CCAGAGGAGAAAGCTGCTTCTCTGATCTTGA		
26883	(240)	CTTCTGCATTTTCTTTTCTGAGGAGAAAGCTGCTTCTCTGATCTTGA		
Consensus	(1185)	GAAATGGGCACA CCACAGGAGAAAGCTGTTGTCTCTGATCTTGA		
		1235		1284
VMP1	(1220)	AAAGTTGCTTCTCTGATCTTGAAGGCTGCTTACTTCTATCTATCATTAAGCT		
22793	(289)	AAAGTTGCTTCTCTGATCTTGAAGGCTGCTTACTTCTATCTATCATTAAGCT		
26883	(290)	AAAGTTGCTTCTCTGATCTTGAAGGCTGCTTACTTCTATCTATCATTAAGCT		
Consensus	(1235)	AAAGTTGCTTCTTGTCTATGCTGCTTACTTCTATCTATCATTAAGCT		
		1285		1334
VMP1	(1270)	CCATGGCACAAGGTTATGCCAAACGAATCCAGCAGCGGTTGAACTCAGAG		
22793	(339)	CCATGGCACAAGGTTATGCCAAACGAATCCAGCAGCGGTTGAACTCAGAG		
26883	(340)	CCATGGCACAAGGTTATGCCAAACGAATCCAGCAGCGGTTGAACTCAGAG		
Consensus	(1285)	CCATGGCACAAGGTTATGCCAAACGAATCCAGCAGCGGTTGAACTCAGAG		
		1335		1384
VMP1	(1320)	GAGAAACTAAATAAGTAGAGAAAGTTTTAACTGCAGAAATTCGAGTGG		
22793	(389)	GAGAAACTAAATAAGTAGAGAAAGTTTTAACTGCAGAAATTCGAGTGG		
26883	(375)	-----		
Consensus	(1335)	GAGAAACTAAATAAGTAGAGAAAGTTTTAACTGCAGAAATTCGAGTGG		
		1385		1434
VMP1	1370)	ATGGGTTCTGCCTTAATTGGGAGGACTCCAAGCCGGGAAGGAAATTC		
22793	(439)	ATGGGTTCTGCCTTAATTGGGAGGACTCCAAGCCGGGAAGGAAATTC		
26883	(375)	-----		
Consensus	(1385)	ATGGGTTCTGCCTTA ATTGGGAGGACTCCAAGCCGGGAAGGAAATTC		
		1435		1467
VMP1	1420)	CTTTTCCAACCTGTATCAATTTTTACAACTTTT		
22793	(489)	CTTTT-----		
26883	(375)	-----		
Consensus	(1435)	CTTTT		

FIG. 4

WO 03/057926

PCT/US03/00657

5/5

**Spot 22793 mapped to VMP1**

VMP1: 1087 gtgctgtccccgcataggtccatctctgcagaagccatttcaggagtacctggaggctc 1146  
 |||  
 22793: 156 gtgctgtccccgcataggtccatctctgcagaagccatttcaggagtacctggaggctc 215

VMP1: 1147 aacggcagaagcttcaccacaaaagcgaaatgggcacaccacagggagaaaaactggttgt 1206  
 |||  
 22793: 216 aacggcagaagcttcaccacaaaagcgaaatgggcacaccacagggagaaaaactggttgt 275

VMP1: 1207 cctggatgtttgaaaagttggtcggtgtcatggtgtgttacttcattcctatctatcatta 1266  
 |||  
 22793: 276 cctggatgtttgaaaagtcggtcgatgtcatggtgtgttacttcattcctatctatcatta 335

VMP1: 1267 actccatggcacaaagttatgccaaacgaatccagcagcggttgaactcagaggagaaaa 1326  
 |||  
 22793: 336 actccatggcacaaagttatgccaaacgaatccagcagcggttgaactcagaggagaaaa 395

VMP1: 1327 ctaaataagtagagaaagttttaactgcagaaattggagtggatgggttctgccttaaa 1386  
 |||  
 22793: 396 ctaaataagtagagaaagttttaactgcagaaattggagtggatgggttctgccttata 455

VMP1: 1387 ttgggaggactccaagccggaaggaaaaattccctttt 1424  
 |||  
 22793: 456 ttgggaggactccaagccggaaggaaaaattccctttt 493

**Spot 27450 mapped to VMP1**

VMP1: 2330 tgtgttaatgttttctagcatgtactctggtttcaacagacacaaatttatatgttaacc 2389  
 |||  
 27450: 1 tgtgttaatgttttctagcatgtactctggtttcaacagacacaaatttatatgttaacc 60

VMP1: 2390 cagttttcttgccgttctgtaagtgttttattcttagtgatgtttttccattgggatg 2449  
 |||  
 27450: 61 cagttttcttgccgttctgtaagtgttttattcttagtgatgtttttccattgggatg 120

VMP1: 2450 tttttgattgaacttggttcattttgttttgcttgggagggaaaaataaacaattttactttt 2509  
 |||  
 27450: 121 tttttgattgaacttggttcattttgttttgcttgggagggaaaaataaacaattttactttt 180

VMP1: 2510 ttcctt 2515  
 |||  
 27450: 181 ttcctt 186

**Spot 26883 mapped to VMP1**

VMP1: 1187 acagggagaaaaactggttgctcctggatgtttgaaaagttggtcggtgtcatggtgtgta 1246  
 |||  
 26883: 257 acagggagaaaaactggttgctcctggatgtttgaaaagttggtcggtgtcatggtgtgta 316

VMP1: 1247 cttcatcctatctatcattaactccatggcacaaagttatgccaaacgaatccagcag 1304  
 |||  
 26883: 317 cttcatcctatctatcattaactccatggcacaaagttatgccaaacgaatccagcag 374

**FIG. 5**